

MGAGGRMQVSPPSKKSETDTIKRVPCEPPPTVGBELKKAIPPHCFKRSIPRSFSYLIWDIIIIASCFFYYVATTFPPLPHPLSYFANPLYWACQCVLTGV 100
10 20 30 40 50 60 70 80 90 100
MGAGGRMQVSPPSKKSETDNIKRVPCEPPPTVGBELKKAIPPHCFKRSIPRSFSYLIWDIIIIASCFFYYVATTFPPLPHPLSYFANPLYWACQCVLTGV 100
MGAGGRMQVSPPSKKSETDTIKRVPCEPPPTVGBELKKAIPPHCFKRSIPRSFSYLIWDIIIIASCFFYYVATTFPPLPHPLSYFANPLYWACQCVLTGV 100

SEQIDNO12
SEQIDNO16

WVIAHECGHAFSDYQNLDDTVGLIFHSFLLVXYFSWKYSHRRHHSNTGSLERDEVFVPPKKSDIKWYGVKYNLNNPLGRTVMLTVQFTLGNPLYLAFNVSG 200
110 120 130 140 150 160 170 180 190 200
WVIAHKCGHAFSDYQNLDDTVGLIFHSFLLVXYFSWKYSHRRHHSNTGSLERDEVFVPPKKSDIKWYGVKYNLNNPLGRTVMLTVQFTLGNPLYLAFNVSG 200
WVIAHECGHAFSDYQNLDDTVGLIFHSFLLVXYFSWKYSHRRHHSNTGSLERDEVFVPPKKSDIKWYGVKYNLNNPLGRTVMLTVQFTLGNPLYLAFNVSG 200

SEQIDNO12
SEQIDNO16

RPYDGGFACHFHPNAPIYNDREBRLQIYISDAGILAVCYGLFRYAAXQGVASMVCFYGVPLLVNGFLVLTLYLQHTHPSLPHYDSSSENDWLRGALATVDR 300
210 220 230 240 250 260 270 280 290 300
RPYDGGFACHFHPNAPIYNDREBRLQIYISDAGILAVCYGLFRYAAXQGVASMVCFYGVPLLVNGFLVLTLYLQHTHPSLPHYDSSSENDWLRGALATVDR 300
RPYDGGFACHFHPNAPIYNDREBRLQIYISDAGILAVCYGLFRYAAXQGVASMVCFYGVPLLVNGFLVLTLYLQHTHPSLPHYDSSSENDWLRGALATVDR 300

SEQIDNO12
SEQIDNO16

DYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIPILGEYYQFDGTPVVKAMWREAKECITYVEPDRQGEKKGVFWYNNKL 384
310 320 330 340 350 360 370 380
DYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIPILGEYYQFDGTPVVKAMWREAKECITYVEPDRQGEKKGVFWYNNKL 384
DYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIPILGEYYQFDGTPVVKAMWREAKECITYVEPDRQGEKKGVFWYNNKL 384

SEQIDNO12
SEQIDNO16